Application No.: 10/533,054 Docket No.: PRD2009USPCT1

EFS Amendment:

## In the Claims:

Please replace all prior listing of claims with the following listing:

(Currently Amended) A method of diagnosing a <u>depression or stress modulated by corticotropin-releasing hormone (CRH)</u> induced gene expression-profile in an individual said method comprising;

- a) obtaining a biological sample of said individual; and
- b) determine the level of gene transcription of a gene comprising a nucleic acid sequence as set forth in -selected from the group consisting of SEQ ID No.1, SEQ ID No.2, SEQ ID No.3, SEQ ID No.4, SEQ ID NO.5, SEQ ID NO.6, SEQ ID NO.7, SEQ ID No.8, SEQ ID NO.9, SEQ ID H., SEQ ID NO.13, SEQ ID NO.15, SEQ ID NO.17, SEQ ID NO.17, SEQ ID NO.19, SEQ ID NO.21, SEQ ID NO.23, SEQ ID No.25, SEQ ID No.26, SEQ ID No.27, SEQ ID No.27, SEQ ID No.30, SEQ ID No.31, SEQ ID No.31, SEQ ID No.32, SEQ ID No.34, SEQ ID No.36, SEQ ID No.38, SEQ ID No.40; and c) correlating a change in the level of said gene transcription of step b) to depression or stress.
- (Currently Amended) A<u>The</u> method according to claim 1 wherein the biological sample is a bodily fluid or tissue sample.
- (Currently Amended) AThe method according to claim 1 wherein the level of gene transcription is determined for the genes-having consisting of the nucleic acid sequences as set forth in consisting of SEQ ID No.1, SEQ ID No.2, SEQ ID No.3, SEQ ID No.4, SEQ ID No.5, SEQ ID No.6, SEQ ID No.7, SEQ ID No.8, SEQ ID NO.9, SEQ ID No.17, SEQ ID NO.19, SEQ ID NO.21, SEQ ID NO.23, SEQ ID NO.25, SEQ ID No.26, SEQ ID No.27, SEQ ID No.28, SEQ ID No.27, SEQ ID No.28, SEQ ID No.29, SEQ ID No.30, SEQ ID No.31, SEQ ID NO.32, SEQ ID NO.34, SEQ ID No.36, SEQ ID No.38 and SEQ ID No.40.
- (Currently Amended) <u>AThe</u> method according to claim 1 wherein the level of gene transcription is <u>being</u> assessed using a probe which binds to a polynucleotide comprising a nucleic acid sequence <u>as set forth in selected from the group consisting</u> of SEO ID No.1. SEO ID No.2. SEO ID No.3. SEO ID No.4. SEO ID NO.5. SEO ID

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NO.6, SEQ ID No.7, SEQ ID No.8, SEQ ID NO.9, SEQ ID 11, SEQ ID NO.13, SEQ ID NO.15, SEQ ID NO.17, SEQ ID NO.17, SEQ ID NO.21, SEQ ID NO.21, SEQ ID NO.22, SEQ ID No.25, SEQ ID No.26, SEQ ID No.27, SEQ ID No.28, SEQ ID No.29, SEQ ID No.30, SEQ ID No.31, SEQ ID NO.32, SEQ ID NO.34, SEQ ID No.36, SEQ ID No.38, SEQ ID No.36, SEQ ID No.38, SEQ ID No.36, SEQ ID No.36, SEQ ID No.38, SEQ ID No.38, SEQ ID No.36, SEQ ID No.38, SE

 (Currently Amended) A<u>The</u> method according to claim 1 wherein the level of gene expression is determined using microarray technology.

## 6. to 32. Cancel.

- (New) The method according to claim 1, wherein the level of gene expression is determined using nucleic acid amplification technique.
- 34. (New) The method according to claim 1, wherein the level of gene expression is determined using hybridization technique.
- 35. (New) The method according to claim 1, wherein the level of gene expression is determined using immunological technique.
- 36. (New) The method according to claim 1, wherein the level of gene expression is determined using separation technique.